



## SEQUENCE LISTING

<110> Falco, S. Carl  
Cahoon, Rebecca E.

<120> Vitamin B Metabolism Proteins

<130> BB-1201 US DIV

<140> 10/081,301  
<141> 2002-02-20

<150> 60/096,342  
<151> 1998-08-12

<160> 16

<170> Microsoft Office 97

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<212> DNA  
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ctccctggct ttgatgtgga tccaataaaac tctgtacagt ttctaatca tacaggatac 180  
ccaacattta gaggtcaggt tcttaatggc aaacagctt gggaccttat tgaaggactg 240  
gaggaaaatc agttgcttca ttataccat ttattaacag gttatataagg ctcagttcc 300  
tttttagata ctgtgctaca agttgttgag aaattgcgt cagttaatcc tgatcttgta 360  
tatgtttgtg acccagttct aggtgatgaa gaaaaactat atgttcctca ggaggtata 420  
tctgtttatc aacagaaggt tggccagtt gcttcaatgc ttacacctaa ccaattttgaa 480  
gttgaactac ttactggatt gaggatcacc tccgaagaag atgggttgac agcttgtaat 540  
accctccaca gtgccggacc acagaaggtg gttataacta gtgctctt tgaaggtaag 600  
ctgctcccta tcggaagtca caaaaaaaca gaggaacaac agccagaaca atttaagatt 660  
gagataccaa agataacctgc atatttcacg ggaactggag atttgcacac tgctctctta 720  
ctaggatgga gtaataaaata tcctgatagc ctcgagaaag cagcagaact ggcagttcc 780  
agtttgccagg cacttctgaa aagaactgtg gaagactata aaatggccgg ctgcaccca 840  
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<212> PRT  
<213> Zea mays

<400> 2  
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Arg Val Leu Ser Ile Gln Ser His Thr Val Gln Gly Tyr Val Gly Asn  
20 25 30

Lys Ser Ala Val Phe Pro Leu Gln Leu Leu Gly Phe Asp Val Asp Pro  
35 40 45

Ile Asn Ser Val Gln Phe Ser Asn His Thr Gly Tyr Pro Thr Phe Arg  
50 55 60

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27

Gly Gln Val Leu Asn Gly Lys Gln Leu Trp Asp Leu Ile Glu Gly Leu  
65 70 75 80

Glu Glu Asn Gln Leu Leu His Tyr Thr His Leu Leu Thr Gly Tyr Ile  
85 90 95

Gly Ser Val Ser Phe Leu Asp Thr Val Leu Gln Val Val Glu Lys Leu  
100 105 110

Arg Ser Val Asn Pro Asp Leu Val Tyr Val Cys Asp Pro Val Leu Gly  
115 120 125

Asp Glu Gly Lys Leu Tyr Val Pro Gln Glu Val Ile Ser Val Tyr Gln  
130 135 140

Gln Lys Val Val Pro Val Ala Ser Met Leu Thr Pro Asn Gln Phe Glu  
145 150 155 160

Val Glu Leu Leu Thr Gly Leu Arg Ile Thr Ser Glu Glu Asp Gly Leu  
165 170 175

Thr Ala Cys Asn Thr Leu His Ser Ala Gly Pro Gln Lys Val Val Ile  
180 185 190

Thr Ser Ala Leu Ile Glu Gly Lys Leu Leu Leu Ile Gly Ser His Lys  
195 200 205

Lys Thr Glu Glu Gln Gln Pro Glu Gln Phe Lys Ile Glu Ile Pro Lys  
210 215 220

Ile Pro Ala Tyr Phe Thr Gly Thr Gly Asp Leu Thr Thr Ala Leu Leu  
225 230 235 240

Leu Gly Trp Ser Asn Lys Tyr Pro Asp Ser Leu Glu Lys Ala Ala Glu  
245 250 255

Leu Ala Val Ser Ser Leu Gln Ala Leu Leu Lys Arg Thr Val Glu Asp  
260 265 270

Tyr Lys Met Ala Gly Phe Asp Pro Ser Thr Ser Ser Leu Glu Ile Arg  
275 280 285

Leu Ile Gln Ser Gln Asp Glu Ile Arg Asn Pro Thr Val Thr Cys Lys  
290 295 300

Ala Val Lys Tyr Gly Ser  
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<213> Oryza sativa

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 agcaaaggaa caaccaccag aacaatttaa gattgagata cccaagatac ctgcataattt 180  
 cacgggcact ggagatttaa caactgcct tctacttaga tggagtaata aataccctga 240  
 taaccttgg aagggcgctg aactggcggt atccatttgc aaggcaccac taaggagaac 300  
 tggaaagac tataaaagac tgggttgac cctccaacca acacctagag atccgcctgg 360  
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 <212> PRT  
 <213> Oryza sativa

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 1 5 10 15

Gly Pro Arg Lys Val Val Ile Thr Ser Ala Leu Ile Glu Asp Lys Leu  
 20 25 30

Leu Leu Ile Gly Ser His Lys Lys Ala Lys Glu Gln Pro Pro Glu Gln  
 35 40 45

Phe Lys Ile Glu Ile Pro Lys Ile Pro Ala Tyr Phe Thr Gly Thr Gly  
 50 55 60

Asp Leu Thr Thr Ala Leu Leu Gly Trp Ser Asn Lys Tyr Pro Asp  
 65 70 75 80

Asn Leu Gly Glu Gly Ala Glu Leu Ala Val Ser Ile Cys Lys Ala Pro  
 85 90 95

Leu Arg Arg Thr Val Glu Asp Tyr Lys Arg Leu Gly Leu Thr Leu Gln  
 100 105 110

Pro Thr Pro Arg Asp Pro Pro Gly Phe Lys Thr Lys Asp Glu Xaa Xaa  
 115 120 125

Xaa Pro Lys Ile His Ala Ser Cys

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<211> 812  
<212> DNA  
<213> Glycine max

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<220>  
<221> unsure  
<222> (683)  
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<220>  
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<222> (778)

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*61*

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<222> (804)

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aggggtatgt tggtataataa tccgctgtct tccctctgca actactggga tatgtatgtcg 180  
atccaattaa ttccgtgcag ttttgcatac atacaggata tccgacgtt aagggtcagg 240  
ttttgaatgg acagcaactc tggatctaa tgcaggcct tgaaggaaat gatttattgt 300  
tctatactca ctgcataaca ggttatattg gttcagatc ttttctaaac actgtattgc 360  
aagttgtcag caaacttcgg tcaacaaaacc caggctttc gtatgtatgt gatccagtga 420  
tgggtgatga aggaaagctt tatgttcctc aagagctgt atcagtctat cgtgagaagg 480  
ttgttccagt agcttcaatg ttgactccca accagttga agcagaacta ctgacaggct 540  
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cttcaaaggn cataattaca agtataaata tagacgggat tcttctctc attggcagtc 660  
atccaaaaga aaaggagag ccnccngac aatttaagat tgttattcca aaaataacca 720  
gcttatttta cggttacggg anancncatg actgnattcn tcttggttng agcataanta 780  
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<212> PRT

<213> Glycine max

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<222> (178)

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<222> (189)

<223> Xaa = any amino acid

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Val Leu Ser Ile Gln Ser His Thr Val Gln Gly Tyr Val Gly Asn Lys  
20 25 30

Ser Ala Val Phe Pro Leu Gln Leu Leu Gly Tyr Asp Val Asp Pro Ile  
35 40 45

Asn Ser Val Gln Phe Ser Asn His Thr Gly Tyr Pro Thr Phe Lys Gly  
50 55 60

*61*

Gln Val Leu Asn Gly Gln Gln Leu Trp Asp Leu Ile Glu Gly Leu Glu  
65 70 75 80

Gly Asn Asp Leu Leu Phe Tyr Thr His Leu Leu Thr Gly Tyr Ile Gly  
85 90 95

Ser Glu Ser Phe Leu Asn Thr Val Leu Gln Val Val Ser Lys Leu Arg  
100 105 110

Ser Thr Asn Pro Gly Leu Ser Tyr Val Cys Asp Pro Val Met Gly Asp  
115 120 125

Glu Gly Lys Leu Tyr Val Pro Gln Glu Leu Val Ser Val Tyr Arg Glu  
130 135 140

Lys Val Val Pro Val Ala Ser Met Leu Thr Pro Asn Gln Phe Glu Ala  
145 150 155 160

Glu Leu Leu Thr Gly Phe Arg Ile Gln Ser Glu Gly His Gly Arg Glu  
165 170 175

Ala Xaa Arg Leu Leu His Ala Ala Gly Pro Ser Lys Xaa Ile Ile Thr  
180 185 190

Ser Ile Asn Ile  
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<212> DNA  
<213> Triticum aestivum

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atccagttcc acaccgtcca ggggtatgtt ggcaacaaat cggccgtctt tccctgcag 120  
ctccttgct ttgatgtgga tccaataaac tctgtacagt tttctaatca tacaggatac 180  
ccaacattta gagggtcagt tcttaatggc aaacagctct gggaaattat tgaaggactg 240  
gaggaaaatc agctgcttca ttatacccat ttattaacag gttatataagg ctcagtttcc 300  
tttttagata ctgtgctaca agttgtttag aaatttgcgt cagttaatcc tgatcttgta 360  
tatgtttgtg acccagtctc aggtgatgaa gggaaaactat atgttccctca ggagctaata 420  
tctgtttatc aacagaaggt tggccagtt gttcaatgc ttacacctaa ccaatttggaa 480  
gttgaactac ttactggatt gaggatcacc tccgaagaag atggtttgac agcttgtaat 540  
accctccaca gtgccggacc acagaagggt gttataacta gtgctcttata tgaaggtaag 600  
ctgctcccta tcggaagtca caaaaaaaca gaggaacaac agccagaaca atttaaagatt 660  
gagataacca agataacctgc atatttcacg gggactggag atttgacaac tgctcccta 720  
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<212> PRT  
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Lys Ser Ala Val Phe Pro Leu Gln Leu Leu Gly Phe Asp Val Asp Pro  
35 40 45

Ile Asn Ser Val Gln Phe Ser Asn His Thr Gly Tyr Pro Thr Phe Arg  
50 55 60

Gly Ser Val Leu Asn Gly Lys Gln Leu Trp Glu Leu Ile Glu Gly Leu  
65 70 75 80

Glu Glu Asn Gln Leu Leu His Tyr Thr His Leu Leu Thr Gly Tyr Ile  
85 90 95

Gly Ser Val Ser Phe Leu Asp Thr Val Leu Gln Val Val Glu Lys Leu  
100 105 110

Arg Ser Val Asn Pro Asp Leu Val Tyr Val Cys Asp Pro Val Leu Gly  
115 120 125

Asp Glu Gly Lys Leu Tyr Val Pro Gln Glu Leu Ile Ser Val Tyr Gln  
130 135 140

Gln Lys Val Val Pro Val Ala Ser Met Leu Thr Pro Asn Gln Phe Glu  
145 150 155 160

Val Glu Leu Leu Thr Gly Leu Arg Ile Thr Ser Glu Glu Asp Gly Leu  
165 170 175

Thr Ala Cys Asn Thr Leu His Ser Ala Gly Pro Gln Lys Val Val Ile  
180 185 190

Thr Ser Ala Leu Ile Glu Gly Lys Leu Leu Leu Ile Gly Ser His Lys  
195 200 205

Lys Thr Glu Glu Gln Gln Pro Glu Gln Phe Lys Ile Glu Ile Pro Lys  
210 215 220

Ile Pro Ala Tyr Phe Thr Gly Thr Gly Asp Leu Thr Thr Ala Leu Leu  
225 230 235 240

Leu Gly Trp Ser Asn Lys Tyr Pro Asp Ile Leu Glu Gly Gly Tyr Gln  
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<210> 9

<211> 828

<212> DNA

<213> Zea mays

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tcctttaccc tggcacatc aatgtgtgt agaattggaa aagctccatc tggtaaaatt 180  
tcatctctca gggagaacta tatttccctt gaacttcttg agagtcaggat gatgtctgtat 240  
ccatttgcattc agttcattaa atggttgtat gaagcgttca cagccgggtcc cggctctgcgt 300  
gagcccaatg caatggcttt gacaactgcc aacaaggaaag gaaaaccttc ttgcaggatg 360  
gttcttttaa agggagttga taaacaggga ttgttttgtt atacaatattt tggtagccgg 420

33

aaggcgcatg acttgtgtga aaaccctaac gcagcactcc ttttctactg gaatgagatg 480  
aaccgtcagg taagagttga agggtcagtt gagaagggttc cagaagctga atcagataaa 540  
tatttccaca gcccggccacg tggaaagtcag cttggtgcca tagtcagcaa gcagaggtact 600  
gtaattgctg gaagagaagt tcttcaacag gattacaaga aatttggaca aaaaatattct 660  
gatgggagct tgattccaaa acctgaatat tggggtggtc acaaattgac accgacactt 720  
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gaagtagatg ggagcacatc gagaggttgc ccccttga 828

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<212> PRT  
<213> Zea mays

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<222> (25)  
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20 25 30

Asn Gln Leu Arg Asp Phe Ser Ser Ser Phe Thr Leu Gly Thr Ser Met  
35 40 45

Cys Val Arg Ile Gly Lys Ala Pro Ser Val Glu Ile Ser Ser Leu Arg  
50 55 60

Glu Asn Tyr Ile Ser Pro Glu Leu Leu Glu Ser Gln Val Met Ser Asp  
65 70 75 80

Pro Phe Asp Gln Phe Leu Lys Trp Phe Asp Glu Ala Val Thr Ala Gly  
85 90 95

Pro Gly Leu Arg Glu Pro Asn Ala Met Ala Leu Thr Thr Ala Asn Lys  
100 105 110

Glu Gly Lys Pro Ser Ser Arg Met Val Leu Leu Lys Gly Val Asp Lys  
115 120 125

Gln Gly Phe Val Trp Tyr Thr Asn Tyr Gly Ser Arg Lys Ala His Asp  
130 135 140

Leu Cys Glu Asn Pro Asn Ala Ala Leu Leu Phe Tyr Trp Asn Glu Met  
145 150 155 160

Asn Arg Gln Val Arg Val Glu Gly Ser Val Glu Lys Val Pro Glu Ala  
165 170 175

Glu Ser Asp Lys Tyr Phe His Ser Arg Pro Arg Gly Ser Gln Leu Gly  
180 185 190

Ala Ile Val Ser Lys Gln Ser Thr Val Ile Ala Gly Arg Glu Val Leu  
195 200 205

Gln Gln Asp Tyr Lys Lys Leu Glu Gln Lys Tyr Ser Asp Gly Ser Leu  
210 215 220

RSY

Ile Pro Lys Pro Glu Tyr Trp Gly Gly Tyr Lys Leu Thr Pro Thr Leu  
225 230 235 240

Phe Glu Phe Trp Gln Gly Gln Ser Arg Leu His Asp Arg Leu Gln  
245 250 255

Tyr Ser Gln Arg Glu Val Asp Gly Ser Thr Val Trp His Ile Glu Arg  
260 265 270

Leu Ser Pro  
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<210> 11  
<211> 555  
<212> DNA  
<213> Oryza sativa

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tttcttgggg gtagattgt tcccccacct attgtgagca aatataagct tcacatcttctt 120  
ccatatacccg gtacctcaat gtgtgtgaga attggaaaag ctccatctgt tgacatttca 180  
tctctaaagaa gaaattacat cttccctgaa cttctcgagn aacaggtgat gcctgatcca 240  
tttgcataant tcgttagatg gtttgcataat ctgttacgct ggctacgtga accaaatgt 300  
atggtaaca actccgataa ggaggaaaaa cttcgcaaaag aatggcctt aanggngttg 360  
ataaccacgg attttttggg ancaattntg ganccaaaag gacatgatta cctgaaaacca 420  
aatgcngccn gttncantgg aaggaataac ggcagtaaaa taaagtctgt canangtcca 480  
aaaaagactg agatttcaaa cnccanagga ataacttng aatntcacac angcanncat 540  
ctganggant ncagg 555

  
<210> 12  
<211> 110  
<212> PRT  
<213> Oryza sativa

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<222> (74)  
<223> Xaa = any amino acid

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<222> (83)  
<223> Xaa = any amino acid

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Ser Lys Tyr Lys Leu His Leu Pro Pro Tyr Pro Gly Thr Ser Met Cys  
35 40 45  
  
Val Arg Ile Gly Lys Ala Pro Ser Val Asp Ile Ser Ser Leu Arg Arg  
50 55 60  
  
Asn Tyr Ile Ser Pro Glu Leu Leu Glu Xaa Gln Val Met Pro Asp Pro  
65 70 75 80  
  
Phe Asp Xaa Phe Val Arg Trp Phe Asp Glu Leu Leu Arg Trp Leu Arg  
85 90 95  
  
Glu Pro Asn Ala Met Val Asn Asn Ser Asp Lys Glu Gly Lys  
100 105 110

<210> 13  
<211> 864  
<212> DNA

89

<213> Glycine max

<400> 13

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tttgccttccac ctgttattgc agaaaaat aagtttatac ttccaccata tcctggact 180  
tccatgtgtg ttcaatttgg aaggcctcca cgtattgata tctcagctctt aagagagaac 240  
tatatctctc cagaatttctt tgaagagcag gtggaggctg accctttaa tcagtttcat 300  
aaatggtttta atgatgcatt ggctgtgtt ttgaaggaac caaatgctat gtccttgca 360  
actgttaggaa aggacggaaa accctcatca agaatggat tgctaaaagg cttggataag 420  
gaaggattt gttggtacac aaactatgaa agtcgaaagg cacgtgaatt atctgaaaat 480  
ccacgtgcac cacttctttt ttactggat ggtttaaacc ggcaggtacg ggtggaaagg 540  
cctgttcaga aagtctctga tgaggaatca gaacagtatt tccatagccg ccctagaggt 600  
agtcaagttt gggcaatagt cagcaagcag agtactgtat tgccggtag gcatgttctt 660  
tatcaggagt acaaagagct ggaagaaaaa tactctgtat gaagtttaat ccctaaacct 720  
aagaactggg gtggatatac gctaaccacca caactttcg agtttggca agggcagaaa 780  
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aaggttgacc ggtggctcc ttga 864

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<212> PRT

<213> Glycine max

<400> 14

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Leu Val Ser Leu Thr Ala Pro Arg Leu Gly Ala Lys Lys Phe Gly Gly  
20 25 30

Pro His His Phe Leu Gly Gly Arg Phe Val Pro Pro Ala Ile Ala Glu  
35 40 45

Lys Tyr Lys Leu Ile Leu Pro Pro Tyr Pro Gly Thr Ser Met Cys Val  
50 55 60

Arg Ile Gly Arg Pro Pro Arg Ile Asp Ile Ser Ala Leu Arg Glu Asn  
65 70 75 80

Tyr Ile Ser Pro Glu Phe Leu Glu Gln Val Glu Ala Asp Pro Phe  
85 90 95

Asn Gln Phe His Lys Trp Phe Asn Asp Ala Leu Ala Ala Gly Leu Lys  
100 105 110

Glu Pro Asn Ala Met Ser Leu Ser Thr Val Gly Lys Asp Gly Lys Pro  
115 120 125

Ser Ser Arg Met Val Leu Leu Lys Gly Leu Asp Lys Glu Gly Phe Val  
130 135 140

Trp Tyr Thr Asn Tyr Glu Ser Arg Lys Ala Arg Glu Leu Ser Glu Asn  
145 150 155 160

Pro Arg Ala Ser Leu Leu Phe Tyr Trp Asp Gly Leu Asn Arg Gln Val  
165 170 175

Arg Val Glu Gly Pro Val Gln Lys Val Ser Asp Glu Glu Ser Glu Gln  
180 185 190

38

Tyr Phe His Ser Arg Pro Arg Gly Ser Gln Ile Gly Ala Ile Val Ser  
195 200 205

Lys Gln Ser Thr Val Val Pro Gly Arg His Val Leu Tyr Gln Glu Tyr  
210 215 220

Lys Glu Leu Glu Glu Lys Tyr Ser Asp Gly Ser Leu Ile Pro Lys Pro  
225 230 235 240

Lys Asn Trp Gly Gly Tyr Arg Leu Thr Pro Gln Leu Phe Glu Phe Trp  
245 250 255

Gln Gly Gln Lys Ser Arg Leu His Asp Arg Leu Gln Tyr Thr Pro His  
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Glu Ile Asn Gly Gln Arg Leu Trp Lys Val Asp Arg Leu Ala Pro  
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Lys Ala His Asp Leu Ser Glu Asn Ser Asn Ala Ala Leu Leu Phe Tyr  
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Trp Asn Glu Met Asn Arg Gln Val Arg Val Glu Gly Ser Val Gln Lys  
35 40 45

Val Ser Glu Glu Glu Ser Glu Lys Tyr Phe His Ser Arg Pro Arg Gly  
50 55 60

Ser Gln Leu Gly Ala Ile Val Ser Lys Gln Ser Thr Val Ile Ser Arg  
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Glu Val Leu Gln Gln Ala Tyr Lys Glu Leu Glu Gln Lys Tyr Ser Asp  
85 90 95

Gly Ser Phe Ile Pro Lys Pro Asp Tyr Trp Gly Gly Tyr Lys Leu Thr  
100 105 110

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Pro Asn Leu Phe Glu Phe Trp Gln Gly Gln Gln Ser Arg Leu His Asp  
115 120 125

Arg Leu Gln Tyr Ser Gln Arg Glu Leu Gly Gly Ser Thr Glu Trp His  
130 135 140

Ile Gln Arg Leu Ser Pro  
145 150

BL

WT